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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/766,363

DATE: 09/17/2004

TIME: 10:37:11

Input Set : N:\Crf3\RULE60\10766363.raw

Output Set: N:\CRF4\09172004\J766363.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Gregory, Richard J.
 3 Wills, Ken N.
 4 Maneval, Daniel C.

5 (ii) TITLE OF INVENTION: Recombinant Adenoviral Vector and
 6 Methods of Use

7 (iii) NUMBER OF SEQUENCES: 9

8 (iv) CORRESPONDENCE ADDRESS:

9 (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 10 (B) STREET: Two Embarcadero Center, Eighth Floor
 11 (C) CITY: San Francisco
 12 (D) STATE: California
 13 (E) COUNTRY: USA
 14 (F) ZIP: 94111-3834

15 (v) COMPUTER READABLE FORM:

16 (A) MEDIUM TYPE: Floppy disk
 17 (B) COMPUTER: IBM PC compatible
 18 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 19 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

20 (vi) CURRENT APPLICATION DATA:

C--> 21 (A) APPLICATION NUMBER: US/10/766,363
 C--> 22 (B) FILING DATE: 27-Jan-2004
 W--> 27 (C) CLASSIFICATION:

C--> 28 (vii) PRIOR APPLICATION DATA:

W--> 25 (A) APPLICATION NUMBER: US/08/328,673
 26 (B) FILING DATE: 25-Oct-1994
 W--> 29 (A) APPLICATION NUMBER: US 08/142,669
 30 (B) FILING DATE: 25-OCT-1993
 W--> 31 (A) APPLICATION NUMBER: US 08/233,669
 32 (B) FILING DATE: 26-APR-1994

C--> 33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Smith, Timothy S.
 35 (B) REGISTRATION NUMBER: 35,367
 36 (C) REFERENCE/DOCKET NUMBER: 016930-000920US

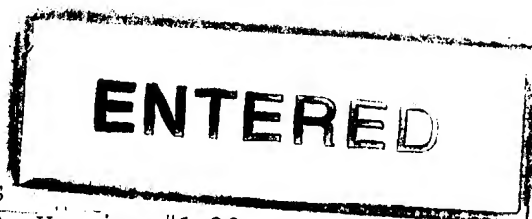
C--> 37 (ix) TELECOMMUNICATION INFORMATION:

38 (A) TELEPHONE: (415) 576-0200
 39 (B) TELEFAX: (415) 576-0300

40 (2) INFORMATION FOR SEQ ID NO: 1:

41 (i) SEQUENCE CHARACTERISTICS:

42 (A) LENGTH: 25 base pairs
 43 (B) TYPE: nucleic acid
 44 (C) STRANDEDNESS: single



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45          (D) TOPOLOGY: linear
W--> 46      (ii) MOLECULE TYPE: DNA
47          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
48          CGCCACCGAG GGACCTGAGC GAGTC
50 (2) INFORMATION FOR SEQ ID NO: 2:
51      (i) SEQUENCE CHARACTERISTICS:
52          (A) LENGTH: 20 base pairs
53          (B) TYPE: nucleic acid
54          (C) STRANDEDNESS: single
55          (D) TOPOLOGY: linear
W--> 56      (ii) MOLECULE TYPE: DNA
57          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
58          TTCTGGGAAG GGACAGAAGA
60 (2) INFORMATION FOR SEQ ID NO: 3:
61      (i) SEQUENCE CHARACTERISTICS:
62          (A) LENGTH: 25 base pairs
63          (B) TYPE: nucleic acid
64          (C) STRANDEDNESS: single
65          (D) TOPOLOGY: linear
W--> 66      (ii) MOLECULE TYPE: DNA
67          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
68          CGCGCTAGCT CTGCCCAAAG GAGCT
70 (2) INFORMATION FOR SEQ ID NO: 4:
71      (i) SEQUENCE CHARACTERISTICS:
72          (A) LENGTH: 39 base pairs
73          (B) TYPE: nucleic acid
74          (C) STRANDEDNESS: single
75          (D) TOPOLOGY: linear
W--> 76      (ii) MOLECULE TYPE: DNA
77          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
78          CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGAAG
80 (2) INFORMATION FOR SEQ ID NO: 5:
81      (i) SEQUENCE CHARACTERISTICS:
82          (A) LENGTH: 35 base pairs
83          (B) TYPE: nucleic acid
84          (C) STRANDEDNESS: single
85          (D) TOPOLOGY: linear
W--> 86      (ii) MOLECULE TYPE: DNA
87          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
88          CGTGCGGCCG CTGGAGGACT TTGAGGATGT CTGTC
90 (2) INFORMATION FOR SEQ ID NO: 6:
91      (i) SEQUENCE CHARACTERISTICS:
92          (A) LENGTH: 33 base pairs
93          (B) TYPE: nucleic acid
94          (C) STRANDEDNESS: single
95          (D) TOPOLOGY: linear
W--> 96      (ii) MOLECULE TYPE: DNA
97          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
98          CGCTCTAGAG AGACCAGTTA GGAAGTTTTTC GCA

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100 (2) INFORMATION FOR SEQ ID NO: 7:
101   (i) SEQUENCE CHARACTERISTICS:
102       (A) LENGTH: 2995 base pairs
103       (B) TYPE: nucleic acid
104       (C) STRANDEDNESS: single
105       (D) TOPOLOGY: linear
106   (ii) MOLECULE TYPE: cDNA
107   (ix) FEATURE:
108       (A) NAME/KEY: CDS
109       (B) LOCATION: 139..2925
110       (D) OTHER INFORMATION: /product= "RB"
111 /note= "retinoblastoma tumor suppressor"
112   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
113   TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTTGTAA CGGGAGTCGG GAGAGGACGG      60
114   GCGGTGCCCC GCGTGC GCGC GCGTCGTCCT CCGCGGCGCT CCTCCACAGC TCGCTGGCTC      120
115   CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC      171
116               Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
117                   1               5               10
118   ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC      219
119   Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
120               15               20               25
121   CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT      267
122   Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
123               30               35               40
124   CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA      315
125   Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
126               45               50               55
127   TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG      363
128   Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
129               60               65               70               75
130   TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT      411
131   Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
132               80               85               90
133   ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA      459
134   Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
135               95               100               105
136   GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC      507
137   Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
138               110               115               120
139   ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT      555
140   Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
141               125               130               135
142   ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT      603
143   Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
144               140               145               150               155
145   GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT      651
146   Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
147               160               165               170
148   ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT      699

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149	Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
150	175 180 185	
151	GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	747
152	Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
153	190 195 200	
154	GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	795
155	Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
156	205 210 215	
157	CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	843
158	Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
159	220 225 230 235	
160	AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	891
161	Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
162	240 245 250	
163	ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	939
164	Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
165	255 260 265	
166	GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	987
167	Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
168	270 275 280	
169	AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	1035
170	Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
171	285 290 295	
172	ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	1083
173	Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
174	300 305 310 315	
175	AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA	1131
176	Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	
177	320 325 330	
178	GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	1179
179	Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
180	335 340 345	
181	ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	1227
182	Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
183	350 355 360	
184	GAA GAG GTG AAT GTA ATT CTT CCA CAC ACT CCA GTT AGG ACT GTT ATG	1275
185	Glu Glu Val Asn Val Ile Leu Pro His Thr Pro Val Arg Thr Val Met	
186	365 370 375	
187	AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	1323
188	Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
189	380 385 390 395	
190	CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1371
191	Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
192	400 405 410	
193	AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1419
194	Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
195	415 420 425	
196	GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1467
197	Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10766363.raw

Output Set: N:\CRF4\09172004\J766363.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:27 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:28 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:31 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)
L:33 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:37 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:46 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:56 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:66 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
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